IN THE SPECIFICATION:

Pursuant to 37 C.F.R. § 1.821-1.825, please incorporate the enclosed paper copy of the substitute SEQUENCE LISTING into the application on the page following the Abstract.

Also, pursuant to 37 C.F.R. § 1.121 (as amended to date), please delete the following paragraphs and replace them with the following replacement paragraphs. It is respectfully submitted that the substitute paragraphs do not introduce new matter into the above-referenced application.

Please delete paragraph **[0020]** and replace it with the following replacement paragraph **[0020]**:

[0020] FIG. 1: Junction sequences of T-DNA and *S. cerevisiae* genomic DNA. *S. cerevisiae* YPH250 (WT), *rad50*, *mre11* and *xrs2* strains were cocultivated with LBA1119(pSDM8000) (SEQ ID NOS: 10-22). G418-resistant colonies were obtained. Chromosomal DNA was isolated and subjected to Vectorette PCR to determine the sequence of genomic DNA flanking the T-DNA. The position of T-DNA integration was determined by basic BLAST search of the yeast genome at http:/www.genome-stanford.edu/SGD. The Watson strand of genomic DNA that is fused to the LB or RB is shown in italics. Bold sequences represent sequence homology between the LB and target site. The filler DNA sequence is underlined and depicted in italics. The numbers above the LB sequences represent the number of bp deleted from the LB. Tel. = telomeric, Subtel. = subtelomeric and Int. = intergenic.

Please delete paragraph **[0021]** and replace it with the following replacement paragraph **[0021]**:

[0021] FIG. 2: Alignment of KU70 homologues. Sc = *Saccharomyces cerevisiae* (SEQ ID NO: 23), Hs = *Homo sapiens* (SEQ ID NO: 24) and At = *Arabidopsis thaliana* (SEQ ID NO: 25). Perfect identity is depicted as black boxes, homology is depicted as grey boxes and dashes are used to optimize alignment.

Please delete paragraph **[0022]** and replace it with the following replacement paragraph **[0022]**:

[0022] FIG. 3: Alignment of *LIG4* homologues. Sc = *Saccharomyces cerevisiae* (SEQ ID NO: 26), Hs = *Homo sapiens* (SEQ ID NO: 27) and At = *Arabidopsis thaliana* (SEQ ID NO: 28). Perfect identity is depicted as black boxes, homology is depicted as grey boxes and dashes are used to optimize alignment.

Please delete paragraph **[0023]** and replace it with the following replacement paragraph **[0023]**:

[0023] FIG. 4: Alignment of *MRE11* homologues. Sc = *Saccharomyces cerevisiae* (SEQ ID NO: 29), Hs = *Homo sapiens* (SEQ ID NO: 30) and At = *Arabidopsis thaliana* (SEQ ID NO: 31). Perfect identity is depicted as black boxes, homology is depicted as grey boxes and dashes are used to optimize alignment.

Please delete paragraph **[0024]** and replace it with the following replacement paragraph **[0024]**:

[0024] FIG. 5: Alignment of *RAD50* homologues. Sc = *Saccharomyces cerevisiae* (SEQ ID NO: 32), Hs = *Homo sapiens* (SEQ ID NO: 33) and At = *Arabidopsis thaliana* (SEQ ID NO: 34). Perfect identity is depicted as black boxes, homology is depicted as grey boxes and dashes are used to optimize alignment.

Please delete paragraph **[0025]** and replace it with the following replacement paragraph **[0025]**:

[0025] FIG. 6: Alignment of XRCC4 homologues. Sc = *Saccharomyces cerevisiae* (SEQ ID NO: 37), Hs = *Homo sapiens* (SEQ ID NO: 36) and At = *Arabidopsis thaliana* (SEQ ID NO: 35).

Please delete paragraph **[0026]** and replace it with the following replacement paragraph **[0026]**:

[0026] The yeast strains that were used are listed in Table 1. Yeast mutants isogenic to the haploid YPH250 strain were constructed using the one-step disruption method (Rothstein, 1991). A 1987 bp fragment from the *YKU70* locus was amplified by PCR using the primers hdflpl 5'-GGGATTGCTTTAAGGTAG-3' (SEQ ID NO: 1) and hdflp2 5'-CAAATACCCTACCCTACC-3' (SEQ ID NO: 2). The PCR product was cloned into pT7Blue (Novagen) to obtain pT7Blue*YKU70*. An 1177 bp *EcoRV*/*Hind*III fragment from the *YKU70* ORF was replaced by a 2033 bp *Hind*III/*Sma*I *LEU2*-containing fragment from pJJ283 (Jones and Prakash, 1990), to form pT7Blue*YKU70::LEU2*. In order to obtain *YKU70* disruptants, Leu^+ colonies were selected after transformation of YPH250 with a 2884 bp *Nde*I/*Sma*I fragment from pT7B1ue*YKU70::LEU2*. The Expand™ High Fidelity System (Boehringer Mannheim) was used according to the supplied protocol to amplify a 3285 bp fragment from the *LIG4* locus with primers dnl4p1 5'-CGTAAGATTCGCCGAGTATAG-3' (SEQ ID NO: 3) and dnl4p2 5'-CGTTTCAAATGGGACCACAGC-3' (SEQ ID NO: 4). The PCR product was cloned into pGEMT (Promega), resulting in pGEMT*LIG4*. A 1326 bp *Bam*HI/*Xho*I fragment from pJJ215 (Jones and Prakash, 1990) containing the *HIS3* gene was inserted into the *Bam*HI and *Xho*I sites of pIC20R, resulting in pIC20R*HIS3*. A 782 bp *Eco*RI fragment from the *LIG4* ORF was replaced with a 1367 bp EcoRI *HIS3*-containing fragment from pIC20R*HIS3* to construct pGEMT*LIG4::HIS3*. In order to obtain *LIG4* disruptants, His^+ colonies were selected after transformation of YPH250 with a 3854 bp *Nco*I/*Not*I fragment from pGEMT*LIG4::HIS3*. In order to obtain *RAD50* disruptants, YPH250 was transformed with an *Eco*RI/*Bgl*II fragment from pNKY83, and Ura^+ colonies were selected (Alani et al., 1989). A *rad50::hisG* strain was obtained by selecting Ura^- colonies on selective medium containing 5-FOA. Similarly, *RAD51* disruptants were obtained after transformation of YPH250 with a *RAD51::LEU2 Xba*I/*Pst*I fragment from pDG152 and selection of Leu^+ colonies (Schiestl et al., 1994). The *TRP1* marker in pSM21 (Schild et al., 1983) was replaced with a *Bgl*II/*Xba*I *LEU2*-containing fragment from pJJ283 (Jones and Prakash, 1990). This resulted in pSM21*LEU2*. Leu^+ *RAD52* disruptant colonies were selected after transformation of YPH250 with the *RAD52::LEU2 Bam*HI fragment

from pSM21*LEU2*. Disruption constructs were transformed to YPH250 by the lithium acetate transformation method as described (Gietz et al., 1992; Schiestl et al., 1993). Disruption of *YKU70*, *LIG4*, *RAD50*, *RAD51* and *RAD52* was confirmed by PCR and Southern blot analysis.

Please delete paragraph **[0030]** and replace it with the following replacement paragraph **[0030]**:

[0030] Chromosomal DNA was isolated using Qiagen's Genomic Tips G/20 per manufacturer's protocol. 1-2 µg of Genomic DNA was digested with *Eco*RI, *Cla*I, *Pst*I or *Hind*III and run on a 1% TBE-gel. Nonradioactive Southern blotting was performed. The membrane was hybridized with a digoxigenine-labeled *kanMX* probe to determine the size of T-DNA/genomic DNA fragments (*Eco*RI and *Cla*I for RB-containing fragments and *Pst*I and *Hind*III for LB-containing fragments). The *kanMX* probe, a 792 bp internal fragment of the *KanMX* marker, was made by PCR using primers *kan*mxp1 5'-AGACTCACGTTTCGAGGCC-3' (SEQ ID NO: 5) and *kan*mxp2 5'-TCACCGAGGCAGTTCCATAG-3' (SEQ ID NO: 6) and a Nonradioactive DNA Labeling and Detection kit (Boehringer Mannheim). The enzyme showing the smallest band on blot was used for Vectorette PCR in order to amplify the smallest junction sequence of T-DNA and genomic DNA. Vectorette PCR was performed as described (http://genomewww.stanford.edu/group/botlab/protocols/vectorette.html). The Expand™ High Fidelity System (Boehringer Mannheim) was used to amplify fragments larger than 2.5 kb, whereas sTaq DNA polymerase (SphaeroQ) was used for amplification of fragments smaller than 2.5 kb. Primers *kan*mxp3 5'-TCGCAGGTCTGCAGCGAGGAGC-3' (SEQ ID NO: 7) and *kan*mxp4 5'-TCGCCTCGACATCATCTGCCCAG-3' (SEQ ID NO: 8) were used to amplify RB/genomic DNA and LB/genomic DNA junction sequences, respectively.

Please delete paragraph **[0031]** and replace it with the following replacement paragraph **[0031]**:

[0031] Vectorette PCR products were cloned in pGEMTEasy (Promega) and sequenced using the T7 polymerase sequencing kit (Pharmacia) according to the manufacturer's protocol. In order to obtain sequences flanking the RB and LB, primers *kan*mxp5

5′-TCACATCATGCCCCTGAGCTGC-3′ (SEQ ID NO: 9) and *kan*mxp4 were used, respectively.